

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/014,501

DATE: 01/04/2002
TIME: 09:57:34

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\01042002\J014501.raw

p5

3 <110> APPLICANT: MERKULOV, Gennady et al.
5 <120> TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
6 NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
7 USES THEREOF

9 <130> FILE REFERENCE: CL001177DIV2

11 <140> CURRENT APPLICATION NUMBER: US/10/014,501

12 <141> CURRENT FILING DATE: 2001-12-14

14 <150> PRIOR APPLICATION NUMBER: 09/813,819

15 <151> PRIOR FILING DATE: 2001-03-22

17 <150> PRIOR APPLICATION NUMBER: 09/920,048

18 <151> PRIOR FILING DATE: 2001-08-02

20 <160> NUMBER OF SEQ ID NOS: 4

22 <170> SOFTWARE: FastSEQ for Windows Version 4.0

24 <210> SEQ ID NO: 1

25 <211> LENGTH: 2968

26 <212> TYPE: DNA

27 <213> ORGANISM: Homo sapiens

29 <400> SEQUENCE: 1

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31 cggagcgccg ctgccatgcg gctggcgctg ctctgggccc tggggctcct gggcgcgggc 120
32 agccctctgc ctccctggcc gctcccaaat atagccctgc tgtcgattcc ctcagtactg 180
33 tcttgggggtg tcctgggacc tgcaggtggc actgaggagc agcaggcaga gtcagagaag 240
34 gccccgaggg agcccttga gccccaggtc ctccaggacg atctcccaat tagcctcaaa 300
35 aaggtgcttc agaccagtct gcctgagccc ctgaggatca agttggagct ggaagggtgac 360
36 agtcatatcc tggagctgct acagaatagg gagttggctc caggccgccc aaccctggtg 420
37 tggtagcagc ccgatggcac tcgggtggct agtgagggac acactttgga gaactgctgc 480
38 taccagggaa gagtgcgggg atatgcaggc tcctgggtgt ccactctgcac ctgctctggg 540
39 ctacagaggct tgggtgctct gacccagag agaagctata ccctggagca ggggctctgg 600
40 gaccttcagg gtcctcccat tatttcgcga atccagatc tccacctgcc aggccacacc 660
41 tgtgccccta gctggcggga atctgtacac actcagacgc caccagagca cccctggga 720
42 cagcgccaca ttcgcccggag gcgggatgtg gtaacagaga ccaagactgt ggagttggtg 780
43 attgtggctg atcactcgga ggcccagaaa taccgggact tccagcacct gctaaaccgc 840
44 acactggaag tggccctctt gctggacaca ttcttccggc ccctgaatgt acgagtggca 900
45 ctagtgggcc tggaggcctg gacccagcgt gacctgggtg agatcagccc aaaccagct 960
46 gtcaccctcg aaaacttctt ccaactggcg agggcacatt tgcctgctcg attgccccat 1020
47 gacagtggcc agctggtgac tggtaattca ttctctgggc ctacgggtgg catggccatt 1080
48 cagaactcca tctgttctcc tgacttctca ggaggtgtga acatggacca ctccaccagc 1140
49 atcctgggag tcgcctcctc catagcccat gagttgggac acagcctggg cctggaccat 1200
50 gatttgctcg ggaatagctg cccctgtcca ggtccagccc cagccaagac ctgcatcatg 1260
51 gaggcctcca cagacttctt accaggcctg aacttcagca actgcagccg acgggcccctg 1320
52 gagaaagccc tcctggatgg aatgggcagc tgccctcttc aacggctgcc tagcctaccc 1380
53 cctatggctg ctttctgctg aaatatgttt gtggagccgg gcgagcagtg tgactgtggc 1440
54 ttccctgatg actgcgtcga tccctgctgt gattctttga cctgccagct gaggccaggt 1500
55 gcacagtgtg catctgacgg accctgttgt caaaattgcc agctgcgccc gtctggctgg 1560
56 cagtgtcgtc ctaccagagg ggattgtgac ttgcctgaat tctgccaggg agacagctcc 1620
57 cagtgtcccc ctgatgtcag cctaggggat ggcgagccct gcgctggcgg gcaagctgtg 1680
58 tgcattgcag ggcgttgtgc ctccatgccc cagcagtgcc agtcactttg gggacctgga 1740

ENTERED

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59 gccagcccg ctgcgccact ttgcctccag acagctaata ctcggggaaa tgcttttggg 1800
60 agctgtgggc gcaaccccag tggcagttat gtgtcctgca cccctagaga tgccatttgt 1860
61 gggcagctcc agtgccagac aggtaggacc cagcctctgc tgggctccat ccgggatcta 1920
62 ctctgggaga caatagatgt gaatgggact gagctgaact gcagctgggt gcacctggac 1980
63 ctgggcagtg atgtggccca gccctcctg actctgcctg gcacagcctg tggccctggc 2040
64 ctggtgtgta tagaccatcg atgccagcgt gtggatctcc tgggggcaca ggaatgtcga 2100
65 agcaaagtgc atggacatgg ggtctgtgac agcaacaggc actgctactg tgaggagggc 2160
66 tgggcacccc ctgactgcac cactcagctc aaagcaacca gctccctgac cacagggctg 2220
67 ctctcagcc tctgtgtctt attggtcctg gtgatgcttg gtgccagcta ctggtaccgt 2280
68 gcccgctgc accagcgact ctgccagctc aagggaacca cctgccagta cagggcagcc 2340
69 caatctggtc cctctgaacg gccaggacct ccgcagaggg cctgtctggc acgaggcact 2400
70 aaggctagtg ctctcagctt cccggccccc ccttcagggc cgctgccgcc tgacctgtg 2460
71 tccaagagac tccagtctca ggggccagcc aagccccac cccaaggaa gccactgcct 2520
72 gccgacccc agggcggtg cccatcggtg gacctgcccg gccaggggc tggaatcccg 2580
73 cccctagtgg taccctccag accagcgcca ccgcctccga cagtgtcctc gctctacctc 2640
74 tgacctctcc ggaggttccg ctgcctccaa gccggactta gggcttcaag aggcgggctg 2700
75 gccctctgga gtccctacc atgactgaag gcgcagaga ctggcggtgt cttagactc 2760
76 cgggcaccgc cagcgctgt caagcaacac tctgcggacc tgccggcgta gttgcagcg 2820
77 gggcttggg aggggctgg ggttggacgg gattgaggaa ggtccgcaca gcctgtctct 2880
78 gctcagttgc aataaacgtg acatcttggg aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2940
79 aaaaaaaaaa aaaaaaaaaa aaaaaaaa 2968

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81 <210> SEQ ID NO: 2

82 <211> LENGTH: 855

83 <212> TYPE: PRT

84 <213> ORGANISM: Homo sapiens

86 <400> SEQUENCE: 2

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87 Met Arg Leu Ala Leu Leu Trp Ala Leu Gly Leu Leu Gly Ala Gly Ser
88 1 5 10 15
89 Pro Leu Pro Ser Trp Pro Leu Pro Asn Ile Ala Leu Leu Ser Ile Pro
90 20 25 30
91 Ser Val Leu Ser Trp Gly Val Leu Gly Pro Ala Gly Gly Thr Glu Glu
92 35 40 45
93 Gln Gln Ala Glu Ser Glu Lys Ala Pro Arg Glu Pro Leu Glu Pro Gln
94 50 55 60
95 Val Leu Gln Asp Asp Leu Pro Ile Ser Leu Lys Lys Val Leu Gln Thr
96 65 70 75 80
97 Ser Leu Pro Glu Pro Leu Arg Ile Lys Leu Glu Leu Asp Gly Asp Ser
98 85 90 95
99 His Ile Leu Glu Leu Leu Gln Asn Arg Glu Leu Val Pro Gly Arg Pro
100 100 105 110
101 Thr Leu Val Trp Tyr Gln Pro Asp Gly Thr Arg Val Val Ser Glu Gly
102 115 120 125
103 His Thr Leu Glu Asn Cys Cys Tyr Gln Gly Arg Val Arg Gly Tyr Ala
104 130 135 140
105 Gly Ser Trp Val Ser Ile Cys Thr Cys Ser Gly Leu Arg Gly Leu Val
106 145 150 155 160
107 Val Leu Thr Pro Glu Arg Ser Tyr Thr Leu Glu Gln Gly Pro Gly Asp
108 165 170 175
109 Leu Gln Gly Pro Pro Ile Ile Ser Arg Ile Gln Asp Leu His Leu Pro

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110          180          185          190
111 Gly His Thr Cys Ala Leu Ser Trp Arg Glu Ser Val His Thr Gln Thr
112          195          200          205
113 Pro Pro Glu His Pro Leu Gly Gln Arg His Ile Arg Arg Arg Asp
114          210          215          220
115 Val Val Thr Glu Thr Lys Thr Val Glu Leu Val Ile Val Ala Asp His
116 225          230          235          240
117 Ser Glu Ala Gln Lys Tyr Arg Asp Phe Gln His Leu Leu Asn Arg Thr
118          245          250          255
119 Leu Glu Val Ala Leu Leu Leu Asp Thr Phe Phe Arg Pro Leu Asn Val
120          260          265          270
121 Arg Val Ala Leu Val Gly Leu Glu Ala Trp Thr Gln Arg Asp Leu Val
122          275          280          285
123 Glu Ile Ser Pro Asn Pro Ala Val Thr Leu Glu Asn Phe Leu His Trp
124          290          295          300
125 Arg Arg Ala His Leu Leu Pro Arg Leu Pro His Asp Ser Ala Gln Leu
126 305          310          315          320
127 Val Thr Gly Thr Ser Phe Ser Gly Pro Thr Val Gly Met Ala Ile Gln
128          325          330          335
129 Asn Ser Ile Cys Ser Pro Asp Phe Ser Gly Gly Val Asn Met Asp His
130          340          345          350
131 Ser Thr Ser Ile Leu Gly Val Ala Ser Ser Ile Ala His Glu Leu Gly
132          355          360          365
133 His Ser Leu Gly Leu Asp His Asp Leu Pro Gly Asn Ser Cys Pro Cys
134          370          375          380
135 Pro Gly Pro Ala Pro Ala Lys Thr Cys Ile Met Glu Ala Ser Thr Asp
136 385          390          395          400
137 Phe Leu Pro Gly Leu Asn Phe Ser Asn Cys Ser Arg Arg Ala Leu Glu
138          405          410          415
139 Lys Ala Leu Leu Asp Gly Met Gly Ser Cys Leu Phe Glu Arg Leu Pro
140          420          425          430
141 Ser Leu Pro Pro Met Ala Ala Phe Cys Gly Asn Met Phe Val Glu Pro
142          435          440          445
143 Gly Glu Gln Cys Asp Cys Gly Phe Leu Asp Asp Cys Val Asp Pro Cys
144          450          455          460
145 Cys Asp Ser Leu Thr Cys Gln Leu Arg Pro Gly Ala Gln Cys Ala Ser
146 465          470          475          480
147 Asp Gly Pro Cys Cys Gln Asn Cys Gln Leu Arg Pro Ser Gly Trp Gln
148          485          490          495
149 Cys Arg Pro Thr Arg Gly Asp Cys Asp Leu Pro Glu Phe Cys Pro Gly
150          500          505          510
151 Asp Ser Ser Gln Cys Pro Pro Asp Val Ser Leu Gly Asp Gly Glu Pro
152          515          520          525
153 Cys Ala Gly Gly Gln Ala Val Cys Met His Gly Arg Cys Ala Ser Tyr
154          530          535          540
155 Ala Gln Gln Cys Gln Ser Leu Trp Gly Pro Gly Ala Gln Pro Ala Ala
156 545          550          555          560
157 Pro Leu Cys Leu Gln Thr Ala Asn Thr Arg Gly Asn Ala Phe Gly Ser
158          565          570          575

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```

159 Cys Gly Arg Asn Pro Ser Gly Ser Tyr Val Ser Cys Thr Pro Arg Asp
160      580      585      590
161 Ala Ile Cys Gly Gln Leu Gln Cys Gln Thr Gly Arg Thr Gln Pro Leu
162      595      600      605
163 Leu Gly Ser Ile Arg Asp Leu Leu Trp Glu Thr Ile Asp Val Asn Gly
164      610      615      620
165 Thr Glu Leu Asn Cys Ser Trp Val His Leu Asp Leu Gly Ser Asp Val
166 625      630      635      640
167 Ala Gln Pro Leu Leu Thr Leu Pro Gly Thr Ala Cys Gly Pro Gly Leu
168      645      650      655
169 Val Cys Ile Asp His Arg Cys Gln Arg Val Asp Leu Leu Gly Ala Gln
170      660      665      670
171 Glu Cys Arg Ser Lys Cys His Gly His Gly Val Cys Asp Ser Asn Arg
172      675      680      685
173 His Cys Tyr Cys Glu Glu Gly Trp Ala Pro Pro Asp Cys Thr Thr Gln
174      690      695      700
175 Leu Lys Ala Thr Ser Ser Leu Thr Thr Gly Leu Leu Leu Ser Leu Leu
176 705      710      715      720
177 Val Leu Leu Val Leu Val Met Leu Gly Ala Ser Tyr Trp Tyr Arg Ala
178      725      730      735
179 Arg Leu His Gln Arg Leu Cys Gln Leu Lys Gly Pro Thr Cys Gln Tyr
180      740      745      750
181 Arg Ala Ala Gln Ser Gly Pro Ser Glu Arg Pro Gly Pro Pro Gln Arg
182      755      760      765
183 Ala Leu Leu Ala Arg Gly Thr Lys Ala Ser Ala Leu Ser Phe Pro Ala
184      770      775      780
185 Pro Pro Ser Arg Pro Leu Pro Pro Asp Pro Val Ser Lys Arg Leu Gln
186 785      790      795      800
187 Ser Gln Gly Pro Ala Lys Pro Pro Pro Pro Arg Lys Pro Leu Pro Ala
188      805      810      815
189 Asp Pro Gln Gly Arg Cys Pro Ser Gly Asp Leu Pro Gly Pro Gly Ala
190      820      825      830
191 Gly Ile Pro Pro Leu Val Val Pro Ser Arg Pro Ala Pro Pro Pro Pro
192      835      840      845
193 Thr Val Ser Ser Leu Tyr Leu
194      850      855
197 <210> SEQ ID NO: 3
198 <211> LENGTH: 17138
199 <212> TYPE: DNA
200 <213> ORGANISM: Homo sapiens
202 <220> FEATURE:
203 <221> NAME/KEY: misc_feature
204 <222> LOCATION: (1)...(17138)
205 <223> OTHER INFORMATION: n = A,T,C or G
207 <400> SEQUENCE: 3
208 ttgggtgacc ctgggcagtg atcacatctc caagcatcag ttttctcacc tgaaaaaaag 60
209 gagatgataa taacactatc tgccttacat gacaattgaa ttgaattttt tttttttttt 120
210 tgagactaag tctcactctg tgcgccaggc tggagtgagc tggcgtgacg ttggctcact 180
211 gcaacctcca cctccccagt tcaagcgatt ctcgctgcctc agcttcccga gtagctggga 240

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212 ttacaggcac acactaccac gcccggctaa tttagaattg aaataattta tgtacagtat 300
213 cttagtacag gacctgacat tataaacaat gagtggcagc cattcttatt taatcagtc 360
214 taacaaagtt cataaaagt agactgtgtt tgcttagctt tttccctagg gctgggatac 420
215 ccccgagccc catgacacac aataggggcc aaatgaatgt gttgtgaaaa aatgaaaaaac 480
216 aaaaaacaaa aaagaacatg ctgggattcc ttgacagggt cgtgaagcaa actgaatgtg 540
217 aatgcacaga tggaaatgtg ccagacagtc attccaagca gaatgtgcaa agactcagtc 600
218 cacagggaat gcgaagtgcc agggctagtc tcaggagaaa ctggctcaga agagacagct 660
219 ctgaggagg gctaaagtag gaaagaggct agaaaggagc caggtgaggg aaggctctga 720
220 aggccaagcc caagagttct gcctgtctgg caggcagcag ggcctctgga gtttcttggg 780
221 caaagagtgg ctgcttctct ggtaagggtg cctgtggaaa atccctgaca actgtgtaga 840
222 gacatgtcgt gagggatggc agggagcata gtgaactagg tttgtggttt ggaatcaggg 900
223 cccctggggg ccagccaagt tggattgttt actatctgtg tgactttgag agtcacttca 960
224 cctttctcaa ctgtaaagtg gggatagcaa cagtgatagt cgatctggcc tgctcacttc 1020
225 tcagcctcac tgtgagaacc aaataagatg atttacagga aagtgc aaaat gagagttgtg 1080
226 gctgatatcc gcttggagag agcctggagg gtgcacctcc ccattctcca tcacagagtt 1140
227 ggggaggagg gcaccctcgc cctccagggg tttcctttgt ccaaccagc ctccctccaa 1200
228 acgcgggaat tgcaggcct ggcgacttca gacaggaaac gctgtccagt tccccctctt 1260
229 tccgcctcgc ctcccggtct ggcgctaacc ccacctccc aacagcgcca cccgctggcg 1320
230 gatatacctg accgcggtct cccgctcctg cgccgctggc tgtgcggcg ctgctgtgtg 1380
231 tgcaggcac ccgagacgcc cgagtcctac gtgtgcccga cgctggactg cgaggccgtg 1440
232 tactgtggtt cgtgctggga cgacatgcgg cagcgggtgc ccgtctgcac gcccgcgaa 1500
233 gagctctctt cctccgcctt tagtgacagc aacgacgaca ctgcctacgc ggggtgaaga 1560
234 ggcgtcctgc tcgctcttcc gcaccgtcct tcccggttaa taaaatgcc tgtagcttcc 1620
235 acgtgggtcg gggactgggg tgagccgcgc actgcctcgc ctgcagtcgg gaaagcctgc 1680
236 ccgcccagac tctccgagcc aggcgcgcga caggaggcag ggaggccgcg aagctactag 1740
237 ggagggttcc ggacctggcg ccgggtgaag gcgcgcgcgc caagccggtc ggaccgggca 1800
238 ccggtctcca ctccgcacag ttgcggggaa gcggtagcgc tgagcagcgc gggcgtagtg 1860
239 ggcggtgtcc ccgctccgca ggcacccggc gcgcagcggg gcgggctttg ccggggcgcg 1920
240 agcttggctt ggggcccggg gggagggggc gggcccgggg ggggcttgg ggccgcgcgg 1980
241 cgctgctggg ttctccgagg cgacctggcc gccggccgct cctccgcgcg ctgttccgca 2040
242 cttgctgccc tcgcccggcc cggagcgccg ctgccatgcg gctggcgctg ctctggggcc 2100
243 tggggctcct gggcgcgggc agccctctgc ctctctggcc gctcccaaat ataggtgagt 2160
244 cctccgcctg gagtgggtcg gggggcggac tgggaggagg gtgcaggaaa gtcggaaggc 2220
245 attagggtaa tggggccgga cggagaccct gggagagccc agccagagcg cggcccgc 2280
246 tggctccgct tcttgggcct agggcccggg gacttggcga tggggtgaaa agagaaggag 2340
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248 ctttcaggct caggtaccag gtaccgagg gctgtccag cgccacttca agatcgtgat 2460
249 gagagggtcg ctgctcccca ggactggcat ctctgctgct ctggggccta gctaaccgtt 2520
250 ccaccgggtg ccaggggcgt gagcgggcat ggcttgtagg gtttagtgaa gaggattctc 2580
251 tctagcctct attccaggcc tggggccgcc aggcactcct caccctggtg ctgttgccac 2640
252 cagtgcctgg ccgagcggga ggggcccag atgagccagg agaagggaga attggccagg 2700
253 aaagaggctg ggacaccaac tctccttgg aactttcact tccgctgct gtcttggg 2760
254 gggaccgaga gggcagcgcg ggggtggagt tccggaggag agagggccat tgtgtgttg 2820
255 ggggggtggg ggtgctcgag gaggaagcag aggtgttagg cagcgggtgt gcctgactgg 2880
256 gcatgagggt gtttagggag gtgggggtgt ttgactgct caccagaaa tgggcgttcc 2940
257 tggcatctcc gatgtgagcg aaggggaggg tgagcgggca cccggccaca aggccttagc 3000
258 cagtctcgag agggggcggt cctgaagtgg ggggagagtg attgggaggg agtgggaacc 3060
259 gcggagggtc ctgtgagAAC ctgggattgg ccggaagggg acaaggaggg ccacaggctg 3120
260 cgcaagccga aagtctttct tggggacttg tgaatgggtt ggtgggtgga aagccataaa 3180

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→ Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:292 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:293 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:339 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
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L:375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:380 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:381 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:382 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:383 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
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L:390 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:391 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
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L:400 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:401 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:405 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:406 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:407 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

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L:408 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:410 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3